

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Katz, Leonard
Stassi, Diane L.
Summers Jr., Richard G.
Ruan, Xiaoan
Pereda-Lopez, Ana
Kakavas, Stephan J.

(ii) TITLE OF THE INVENTION: NOVEL POLYKETIDE DERIVATIVES
AND RECOMBINANT METHODS FOR MAKING SAME

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Rd.
(C) CITY: Abbott Park
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 16-MAY-1979
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dianne Casuto
(B) REGISTRATION NUMBER: P-40,943
(C) REFERENCE/DOCKET NUMBER: 4952.US.P2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (847)-938-3137
(B) TELEFAX: (847)-938-2623
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCCGCTGG	CGGTGATGTT	CACCGGACAG	GGCTCCCAAC	GCCCCGGCAT	GGGACGACAG	60
TTGTACGAGC	ACTTCCCCT	CTTCGCCAG	GCACGGACG	AGGTCTTCGC	ACTGCCACC	120
CCCGGACTAC	GCGAGGTGAT	TTTCGACCCC	GACCAGGCG	AAACACTCCA	ACGCACCGAC	180
CACGCCAGA	TGCCCCCTGTT	CGCCTTCGAA	ACCGCCCTCT	ACCGACTCTG	GGAATCCTGG	240
GGCCTGCGAC	CCGACATGGT	CTGCGGACAC	TCGGTCGGAG	AAATCACCGC	AGCCCACGTC	300
TCCGGCACCC	TCACCCCTCCC	CGACGCCGTC	CACCTCGTCA	CCACACGCG	CACCCCTCATG	360
CAAAACCTGC	CCCCGGCGG	CGCCATGCTC	GGCGTCGCCA	CGGACCCCCA	CACCCCTCAA	420
CCCCACCTCG	ACAACCACCA	CGACACCATC	TCCATCGCCG	CCATCAACGG	CCCCACGCC	480
ACCGTCCTCT	CCGGGACCG	CACCACCTC	CACCACATCG	CCACCCAACT	CAACACCAA	540
CCCTTCACCA	CCACCCCTAA	CACCCCTCACC	CACCACCCCC	CACACACACC	CCTCATCAGC	600
ATGCTCACCG	CCACACCCAC	CCACCCGAC	ACCACCCACT	GGACCCAGCA	CATCACCGCA	660
CCCGTCCGCT	ACACCGACAC	CCTCCACAC	CTCCACCCACC	ACGGCATCAC	CACCTACCTC	720
GAAATCGGCC	CCGACACCCAC	CCTCACCGCC	CTCGCCCGCA	CCACCCCTCCC	CACCAACACC	780
CACCTCATCC	CCACCAACCG	CGCGAACAC	AACGAAGTCC	GCAGCACGAA	CGAGGGCGTTG	840
GGCAGGGTGT	TCAGCGTGGG	CCACTCGGTG	GACTGGCGGG	CCCTCACTCC	GACCGGGAGG	900
CGTACCTCCC	TGCCGACGTA	CCCGCT				925

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTAGGACGG	CAGTCCTGCT	CACCGGGCAG	GGTTCCCAAGC	GTCAGGGCAT	GGGGCGCGAA	60
CTGTACGACC	GGTCACCGGT	GTTCGCCGCC	TCGTTCGACG	CGATCTCGC	TCAACTCGAC	120
GGGCAACTGC	CTCGTCCCCCT	CAAGGACGTT	CTCTTCGCC	CCGAGGGGTC	GGAGGACGCC	180
GCGCTCATCG	ACCGTACGGT	TTTCACACAG	GCGGCTCTGT	TCGCGGTGGA	GACCTCCCTG	240
TTCCGGCTGT	TCGAGGCCCA	CGGCCTCGTC	CCCGACTTAC	TCATCGGCC	CTCCATCGGC	300
GAAGTGACCG	CGGCCACCT	GGCGGGGTC	CTCGATCTGG	CGGACCGGTG	CGTCCTGGTC	360
GCCCACCGCG	GCCGCTGAT	GCAGTCGGCC	CGGGCCGGCG	GGCGGATGGC	CGCGGTCCAG	420
GCGAGCGAGG	ACGAGGTACG	CGAGGCCCTC	GCGACCTTCG	ACGATGCGGT	TGCCGTGGCC	480
GGAGTCACCG	GCCCGAACCG	CACCGTCGTC	TCCGGCGACG	AGGACCGGT	CGAGCGGTG	540
GTCGCGCGCT	GGCGCGAGCA	GGGCAGGCGG	ACGAAGCGGC	TGCCGTTCAG	CCACGCCCTTC	600
CACTCGCCGC	ACATGGACGG	GATCGTCGAC	GAGTTCGTCA	CCGCGTCTC	GGGCTCACC	660
TTCCGGCTCC	CGACGATCCC	GGTCGTCTCC	AACGTCACCG	GGACCCCTCGC	CACCGTCGAC	720
CAGCTGACCT	CGCCCGCGTA	CTGGGCACGC	CACATCCGG	AGGCGGTGCG	CTTCGCCGAC	780
GGGGTGCCTG	ACCTGGAGGG	CGAGGGCGTC	ACCGAATGGC	TGGAGCTCGG	GCCCGACGGC	840

GTTCTCGTCG	CCCTGGTCGA	GGACTGCCTG	GCGAAGGAGG	CGGGATCGCT	CGCGTCCGCC	900
CTGCGCAAGG	GGCGAGCGA	GCCCCACACC	GTGGGCGCGG	CCATGGCCCG	CGCGGTGCTG	960
CGCGGATCCG	GCCCCGACTG	GGCGGCGGTG	TTCCCCGGCG	CACGGCGGGT	CGACCTTCCG	1020
ACGTATGCAT						1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATCTACACST CSGGCACCSAC SGGCAAGCCS AAGGG

35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTSAAGGCSG GCGGCGCSTA CGTSCCSATC GACCC

35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCGAATTCC TAGGCTGGCG GTGATGTTCA

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

050735056 - 12014200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCCGGATCCA TGCATACGTC GGCAGGGAGG TAC

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTCGAATTG CGTGGTCGCG GTGCACCT

28

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACGGATCCG GCCCTAGGCT GCGCCCGGCT CG

32

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGGGATCCT ATGCATTCCA GCGCGAGCGC

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

098765432109

GAGAAGCTTG GCGCGACTTG CCCGCT

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTTAAGC TTGGTACCTG CTCACCGGCA ACACCG

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTTTTGGAT CCCTGCAGCC TAGGGTCGGA GGCACTGCCG GT

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTTTTCTGC AGTATGCATT CCAGGGCAAG CGGTTCT

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTTTGAAT TCACGGCGTTG CCCGCAGCGT AGGGCG

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCGAATTCCCTAGGACGG CAGTCCTGCT CACC

34

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCGGATCC ATGCATACTGT CGGAAGGTG ACCCG

35

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCGAAGAAC TCCCTAGGGT TGCCTTCCTG TTGAC

36

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCGAAAGC TTATGCATAG ACCGGCAGAT CCACCG

36

(2) INFORMATION FOR SEQ ID NO:19:

009735056 - 420 21 1088

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

19

CGGTSAAAGTC SAACATCGG

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

20

GCRATCTCRC CCTGCGARTG

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

44

GAGAGAGGAA CCAACGCGCA CGTGATCGTC GAAGAGGCAC CAGC

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

45

GAGAGAGGAT CCGACCTAGG CGCGGAGGTC ACCGGCGCGA CGGCG

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

09235056-12011000

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAGAGACCTA GGAAGCCGGT GTTCGTGTTG CCCGGCCAGG GCT

43

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGAGAGGAT CCGAGGCCGG CCGTGCGCCC GGACCGAAGA CCGCCTC

47

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGAGAATTCT CCTAGGGTCG CCTTCGTCTT TCCCGGGCAG G

41

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTGAGATCTT ATGCATACGA GGGAAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs

09735056-4221400

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTGAGATCTT ATGCATACGA GGGAAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTGAGATCTT ATGCATACGA GGGAAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1010 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCGACCGTG	TCGTGTCGT	GTTCCCCGGC	CAGGGCTCGC	AGTGGGCCGG	AATGCCGAG	60
GGGCTGCTGG	AGCGGTCCGG	CGCGTTCCGG	AGTGGGCCGG	ACTCGTGCAG	CGCCCGCCTG	120
CGGCCGTACC	TCGGCTGGTC	GGTGTGAGC	GTGCTGCAGC	GGGAACCGGA	CGCGCCCTCG	180
CTCGACCGGG	TCGACGTCGT	GCAGCCGGTG	CTGTTCACGA	TGATGGTCTC	GCTCCGGCG	240
GTCTGGCGTG	CGCTGGGGGT	GAACCCGGCG	GCCTGCGTCG	GGCACTCGCA	GGGTGAGATC	300
GCCGCTGCC	ATGTCGCCGG	TGCGCTGTCG	CTGGACGACT	CGGCCGGAT	CGTCGCCCTG	360
CGCAGTCGGG	CGTGGCTCGG	ACTGGCGGGC	AAGGGCGGCA	TGGTGGCGGT	GCCGATGCCG	420
GGGGAGGAGC	TGCGGCCGCG	GCTGGTGACG	TGGGGGGACC	GTCTGGCCGT	CGCCGCCGTC	480
AACAGCCCCG	GTTCTGCGC	CGTCGCAGGC	GACCCGGAGG	CGCTGGCCGA	ACTGGTGGCG	540
CTGCTGACCG	GTGAGGGGGT	GCACGCCCGG	CCGATCCCCG	CGTCGACAC	GGCGGGCCAC	600
TCGCGCGAGG	TGGACCGCGTT	CGGGGCTCAT	CTGCTGGAGG	TGCTGGCCCC	GGTCGCC	660
CGACCGGCCG	ACATCCCCTT	CTACTCGACG	GTGACCGCG	GGCTGCTGGA	CGGCACCGAG	720
CTGGACGCGA	CGTACTGGTA	CCGCAACATG	CGCGAGCCCG	TCGAGTTCGA	CGGGGCCACA	780
CGGGCGCTGA	TCGCGCACGG	GCACGACGTC	TTCCTGGAGA	CGAGCCCGCA	TCCCATGCTG	840
GGCGTGGCGC	TGGAGCAGAC	GGTCACCGAC	GCCGGCACCG	ACGCGGCCGT	GCTCGGGACC	900
CTGCGCCGCC	GCCACGGCGG	TCCCTCGCG	CTGGCCCTGG	CCGTCTGCCG	CGCCTTCGCG	960
AGGCGGTCTT	CGGTCCGGGC	GCACGCCCG	TGGAGTTGCC	CACCTATCCG		1010

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGCGCGCCTG	CCTTCGTCTT	TCCCAGGCAG	GGCGCCAGT	GGGCCGGACT	GGGAGCGCGG	60
CTCCCTCGCGG	ACTCCCCGT	CTTCGCGCC	AGGGCCGAGG	CATGCGCGG	GGCGCTGGAG	120
CCTCACCTCG	ACTGGTCGGT	CCTCGACGTG	CTGGCCGGCG	CCCCGGGCAC	CCCTCCCATC	180
GACCGGGCCG	ACGTGGTGCA	GCCGGTGTG	TTCACCACGA	TGGTCTCGCT	GGCCGCCCTC	240
TGGGAGGCC	ACGGGGTGCG	GCCGGCCGCG	GTCGTGGGCC	ACTCCCAGGG	CGAGGTGGCC	300
GCGGCCCTGCG	TGGCCGGTGC	CCTGTCGCTG	GACGACGCTG	CCCTGGTGT	CGCCGGACGC	360
AGCAGGCCTGT	GGGGCGGCT	GGCGGGAAAC	GGCAGGGATGC	TCGCGGTGT	GGCTCCGGCC	420
GAGCGGATCC	GTGAGCTGCT	CGAACCATGG	CGGCAGCGGA	TTTCGGTGGC	GGCGGTCAAT	480
GGCCCCGCT	CGGTACCGT	CTCCGGTGAC	GCGCTCGCGC	TGGAGGAGTT	CGGGCGCGGG	540
CTCTCCGCGG	AGGGGGTGCT	GCGCTGGCCG	CTGCCGGCG	TCGACITTCGC	CGGCCACTCG	600
CCGCAGGTGG	AGGAGTTCCG	CGCTGAGCTC	CTGGACCTGC	TCTCCGGCGT	ACGGCCGGCT	660
CCTTCGCGGA	TACTTTCTT	CTCCACCGTG	ACGGCGGGTC	CTTGC GGCG	CGACCAGCTG	720
GACGGGGCGT	ACTGGTACCG	CAACACCGC	GAACCCGTGG	AGTTTCGACGC	CACGGTCCGG	780
GCGCTGCTGC	GTGCGGGCCA	TCACACGTT	ATCGAGGTGC	GTCCGCA	GCTGCTCAAC	840
GCCCGGATCG	ACGAGATCGC	AGCGGACGAG	GGGGTAGCGG	CCACGGCCCT	GCATACGCTC	900
CAGCGGGGCG	CTGGCGGCCT	TGACCGCGTG	CGAACACCGG	TGGGCGCCGC	TTTCGCGCAC	960
GCTGTCCGGG	TCGACTGGAA	CGCCCTGTTC	GAGGGCACCG	GTGGCGCGAG	GGTGCCGCTT	1020
CCCTCGTACG	CCTTC					1035

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly	Pro	Leu	Ala	Val	Met	Phe	Thr	Gly	Gln	Gly	Ser	Gln	Arg	Pro	Gly
1					5			10					15		
Met	Gly	Arg	Gln	Leu	Tyr	Glu	His	Phe	Pro	Val	Phe	Ala	Gln	Ala	Leu
					20			25					30		
Asp	Glu	Val	Phe	Ala	Leu	Ala	Thr	Pro	Gly	Leu	Arg	Glu	Val	Met	Phe
					35			40				45			
Asp	Pro	Asp	Gln	Ala	Glu	Thr	Leu	Gln	Arg	Thr	Asp	His	Ala	Gln	Ile
					50			55				60			
Ala	Leu	Phe	Ala	Phe	Glu	Thr	Ala	Leu	Tyr	Arg	Leu	Trp	Glu	Ser	Trp
					65			70				75			80
Gly	Leu	Arg	Pro	Asp	Met	Val	Cys	Gly	His	Ser	Val	Gly	Glu	Ile	Thr
					85			90				95			
Ala	Ala	His	Val	Ser	Gly	Thr	Leu	Thr	Leu	Pro	Asp	Ala	Val	His	Leu

09735056-424200

100 105 110
 Val Thr Thr Arg Gly Thr Leu Met Gln Asn Leu Pro Pro Gly Gly Ala
 115 120 125
 Met Leu Ala Val Ala Thr Asp Pro His Thr Leu Gln Pro His Leu Asp
 130 135 140
 Asn His His Asp Thr Ile Ser Ile Ala Ala Ile Asn Gly Pro His Ala
 145 150 155 160
 Thr Val Leu Ser Gly Asp Arg Thr Thr Leu His His Ile Ala Thr Gln
 165 170 175
 Leu Asn Thr Lys Thr Asn Trp Leu Asn Val Ser His Ala Phe His Ser
 180 185 190
 Pro Leu Met Gln Pro Ile Leu Gln Pro Phe Thr Thr Leu Asn Thr
 195 200 205
 Leu Thr His His Pro Pro His Thr Pro Leu Ile Ser Met Leu Thr Ala
 210 215 220
 Thr Pro Thr His Pro Asp Thr Thr His Trp Thr Gln His Ile Thr Ala
 225 230 235 240
 Pro Val Arg Tyr Thr Asp Thr Leu His His Leu His His Gly Ile
 245 250 255
 Thr Thr Tyr Leu Glu Ile Gly Pro Asp Thr Thr Leu Thr Ala Leu Ala
 260 265 270
 Arg Thr Thr Leu Pro Thr Thr His Leu Ile Pro Thr Thr Arg Arg
 275 280 285
 Asn His Asn Glu Val Arg Ser Thr Asn Glu Ala Leu Gly Arg Val Phe
 290 295 300
 Ser Val Gly His Ser Val Asp Trp Arg Ala Leu Thr Pro Thr Gly Arg
 305 310 315 320
 Arg Thr Ser Leu Pro Thr Tyr Pro
 325

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Pro Arg Thr Ala Val Leu Leu Thr Gly Gln Gly Ser Gln Arg Gln Gly
 1 5 10 15
 Met Gly Arg Glu Leu Tyr Asp Arg Ser Pro Val Phe Ala Ala Ser Phe
 20 25 30
 Asp Ala Ile Cys Ala Gln Leu Asp Gly Gln Leu Pro Arg Pro Leu Lys
 35 40 45
 Asp Val Leu Phe Ala Pro Glu Gly Ser Glu Asp Ala Ala Leu Ile Asp
 50 55 60
 Arg Thr Val Phe Thr Gln Ala Ala Leu Phe Ala Val Glu Thr Ser Leu
 65 70 75 80
 Phe Arg Leu Phe Glu Ala His Gly Leu Val Pro Asp Tyr Leu Ile Gly

85	90	95	
His Ser Ile Gly Glu Val Thr Ala Ala His	Leu Ala Gly Val Leu Asp		
100	105	110	
Leu Ala Asp Ala Cys Val Leu Val Ala His	Arg Gly Arg Leu Met Gln		
115	120	125	
Ser Ala Arg Ala Gly Gly Ala Met Ala Ala Val	Gln Ala Ser Glu Asp		
130	135	140	
Glu Val Arg Glu Ala Leu Ala Thr Phe Asp Asp	Ala Val Ala Val Ala		
145	150	160	
Gly Val Asn Gly Pro Asn Ala Thr Val Val Ser	Gly Asp Glu Asp Ala		
165	170	175	
Val Glu Arg Leu Val Ala Arg Trp Arg Glu Gln	Gly Arg Arg Thr Lys		
180	185	190	
Arg Leu Pro Val Ser His Ala Phe His Ser Pro	His Met Asp Gly Ile		
195	200	205	
Val Asp Glu Phe Val Thr Ala Val Ser Gly Leu	Thr Phe Arg Ser Pro		
210	215	220	
Thr Ile Pro Val Val Ser Asn Val Thr Gly Thr	Leu Ala Thr Val Asp		
225	230	235	240
Gln Leu Thr Ser Pro Ala Tyr Trp Ala Arg His	Ile Arg Glu Ala Val		
245	250	255	
Arg Phe Ala Asp Gly Val Arg Tyr Leu Glu Gly	Val Thr Glu		
260	265	270	
Trp Leu Glu Leu Gly Pro Asp Gly Val Leu Val	Ala Leu Val Glu Asp		
275	280	285	
Cys Leu Ala Lys Glu Ala Gly Ser Leu Ala Ser	Ala Leu Arg Lys Gly		
290	295	300	
Ala Ser Glu Pro His Thr Val Gly Ala Ala Met	Ala Arg Ala Val Leu		
305	310	315	320
Arg Gly Ser Gly Pro Asp Trp Ala Ala Val Phe	Pro Gly Ala Arg Arg		
325	330	335	
Val Asp Leu Pro Thr Tyr Ala			
340			

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Asp Arg Val Val Phe Val Phe Pro Gly Gln	Gly Ser Trp Ala		
1	5	10	15
Gly Met Ala Glu Gly Leu Leu Glu Arg Ser	Gly Ala Phe Arg Ser Ala		
20	25	30	
Ala Asp Ser Cys Asp Ala Ala Leu Arg Pro	Tyr Leu Gly Trp Ser Val		
35	40	45	
Leu Ser Val Leu Arg Gly Glu Pro Asp Ala	Pro Ser Leu Asp Arg Val		

50 55 60
 Asp Val Val Gln Pro Val Leu Phe Thr Met Met Val Ser Leu Ala Ala
 70 75 80
 65 Val Trp Arg Ala Leu Gly Val Glu Pro Ala Ala Val Val Gly His Ser
 85 90 95
 Gln Gly Glu Ile Ala Ala Ala His Val Ala Gly Ala Leu Ser Leu Asp
 100 105 110
 Asp Ser Ala Arg Ile Val Ala Leu Arg Ser Arg Ala Trp Leu Gly Leu
 115 120 125
 Ala Gly Lys Gly Gly Met Val Ala Val Pro Met Pro Ala Glu Glu Leu
 130 135 140
 Arg Pro Arg Leu Val Thr Trp Gly Asp Arg Leu Ala Val Ala Val
 145 150 155 160
 Asn Ser Pro Gly Ser Cys Ala Val Ala Gly Asp Pro Glu Ala Leu Ala
 165 170 175
 Glu Leu Val Ala Leu Leu Thr Gly Glu Gly Val His Ala Arg Pro Ile
 180 185 190
 Pro Gly Val Asp Thr Ala Gly His Ser Pro Gln Val Asp Ala Leu Arg
 195 200 205
 Ala His Leu Leu Glu Val Leu Ala Pro Val Ala Pro Arg Pro Ala Asp
 210 215 220
 Ile Pro Phe Tyr Ser Thr Val Thr Gly Gly Leu Leu Asp Gly Thr Glu
 225 230 235 240
 Leu Asp Ala Thr Tyr Trp Tyr Arg Asn Met Arg Glu Pro Val Glu Phe
 245 250 255
 Glu Arg Ala Thr Arg Ala Leu Ile Ala Asp Gly His Asp Val Phe Leu
 260 265 270
 Glu Thr Ser Pro His Pro Met Leu Ala Val Ala Leu Glu Gln Thr Val
 275 280 285
 Thr Asp Ala Gly Thr Asp Ala Ala Val Leu Gly Thr Leu Arg Arg Arg
 290 295 300
 His Gly Gly Pro Arg Ala Leu Ala Leu Ala Val Cys Arg Ala Phe Ala
 305 310 315 320
 His Gly Val Glu Val Asp Pro Glu Ala Val Phe Gly Pro Gly Ala Arg
 325 330 335
 Pro Val Glu Leu Pro Thr Tyr Pro
 340

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Ala Pro Ala Phe Val Phe Pro Gly Gln Gly Ala Gln Trp Ala Gly
 1 5 10 15
 Leu Gly Ala Arg Leu Leu Ala Asp Ser Pro Val Phe Arg Ala Arg Ala

30

Glu Ala Cys Ala Arg Ala Leu Glu Pro His Leu Asp Trp Ser Val Leu	20	25	30
Asp Val Leu Ala Gly Ala Pro Gly Thr Pro Pro Ile Asp Arg Ala Asp	35	40	45
Val Val Gln Pro Val Leu Phe Thr Thr Met Val Ser Leu Ala Ala Leu	50	55	60
Trp Glu Ala His Gly Val Arg Pro Ala Ala Val Val Gly His Ser Gln	65	70	75
Gly Glu Val Ala Ala Cys Val Ala Gly Ala Leu Ser Leu Asp Asp	85	90	95
Ala Ala Leu Val Ile Ala Gly Arg Ser Arg Leu Trp Gly Arg Leu Ala	100	105	110
Gly Asn Gly Gly Met Leu Ala Val Met Ala Pro Ala Glu Arg Ile Arg	115	120	125
Glu Leu Leu Glu Pro Trp Arg Gln Arg Ile Ser Val Ala Ala Val Asn	130	135	140
Gly Pro Ala Ser Val Thr Val Ser Gly Asp Ala Leu Ala Leu Glu Glu	145	150	155
Phe Gly Ala Arg Leu Ser Ala Glu Gly Val Leu Arg Trp Pro Leu Pro	165	170	175
Gly Val Asp Phe Ala Gly His Ser Pro Gln Val Glu Glu Phe Arg Ala	180	185	190
Glu Leu Leu Asp Leu Leu Ser Gly Val Arg Pro Ala Pro Ser Arg Ile	195	200	205
Pro Phe Phe Ser Thr Val Thr Ala Gly Pro Cys Gly Gly Asp Gln Leu	210	215	220
Asp Gly Ala Tyr Trp Tyr Arg Asn Thr Arg Glu Pro Val Glu Phe Asp	225	230	235
Ala Thr Val Arg Ala Leu Leu Arg Ala Gly His His Thr Phe Ile Glu	245	250	255
Val Gly Pro His Pro Leu Leu Asn Ala Ala Ile Asp Glu Ile Ala Ala	260	265	270
Asp Glu Gly Val Ala Ala Thr Ala Leu His Thr Leu Gln Arg Gly Ala	275	280	285
Gly Gly Leu Asp Arg Val Arg Asn Ala Val Gly Ala Ala Phe Ala His	290	295	300
Gly Val Arg Val Asp Trp Asn Ala Leu Phe Glu Gly Thr Gly Ala Arg	305	310	315
Arg Val Pro Leu Pro Ser Tyr Ala Phe	325	330	335
	340	345	

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